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| APPLICATION NO. | FILING DATE | FIRST NAMED INVENTOR | ATTORNEY DOCKET NO. | CONFIRMATION NO | | | | | | |
|-----------------|----------------------------------------|----------------------|------------------------|-------------------------|--|--|--|--|--|--|
| 10/824,581 | 04/14/2004 | Arie Ben-Bassat | CL2371 USNA | 7161 | | | | | | |
| 23906 | 7590 12/05/2006 | | EXAM | INER | | | | | | |
| | IT DE NEMOURS ANI | RAMIREZ, | RAMIREZ, DELIA M | | | | | | | |
| | ENT RECORDS CENTEI LL PLAZA 25/1128 | · · | ART UNIT | PAPER NUMBER | | | | | | |
| 4417 LANCA | | | 1652 | | | | | | | |
| WILMINGTO | ON, DE 19805 | | DATE MAILED: 12/05/200 | DATE MAILED: 12/05/2006 | | | | | | |

Please find below and/or attached an Office communication concerning this application or proceeding.

| | Application No. | Applicant(s) | | | | | | | | | | |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------|--|--|--|--|--|--|--|--|--|--|
| | 10/824,581 | BEN-BASSAT ET AL. | | | | | | | | | | |
| Office Action Summary | Examiner | Art Unit | | | | | | | | | | |
| · | Delia M. Ramirez | 1652 | | | | | | | | | | |
| The MAILING DATE of this communication app | ears on the cover sheet with the c | orrespondence address | | | | | | | | | | |
| Period for Reply | | | | | | | | | | | | |
| A SHORTENED STATUTORY PERIOD FOR REPLY WHICHEVER IS LONGER, FROM THE MAILING DA - Extensions of time may be available under the provisions of 37 CFR 1.13 after SIX (6) MONTHS from the mailing date of this communication. - If NO period for reply is specified above, the maximum statutory period w - Failure to reply within the set or extended period for reply will, by statute, Any reply received by the Office later than three months after the mailing earned patent term adjustment. See 37 CFR 1.704(b). | ATE OF THIS COMMUNICATION 36(a). In no event, however, may a reply be tim vill apply and will expire SIX (6) MONTHS from a cause the application to become ABANDONE | J. lely filed the mailing date of this communication. O (35 U.S.C. § 133). | | | | | | | | | | |
| Status | | | | | | | | | | | | |
| 1) Responsive to communication(s) filed on 25 Se | entember 2006 | | | | | | | | | | | |
| | action is non-final. | | | | | | | | | | | |
| 3) Since this application is in condition for allowar | | secution as to the merits is | | | | | | | | | | |
| | closed in accordance with the practice under <i>Ex parte Quayle</i> , 1935 C.D. 11, 453 O.G. 213. | | | | | | | | | | | |
| Disposition of Claims | • | | | | | | | | | | | |
| 4)⊠ Claim(s) <u>1-40</u> is/are pending in the application. | | | | | | | | | | | | |
| 4a) Of the above claim(s) is/are withdray | | | | | | | | | | | | |
| 5) Claim(s) is/are allowed. | | | | | | | | | | | | |
| 6) Claim(s) <u>1-14,17-19,25,29 and 38-40</u> is/are rej | ected. | | | | | | | | | | | |
| 7) Claim(s) 15,16,20-24,26-28 and 30-37 is/are of | | • | | | | | | | | | | |
| 8) Claim(s) are subject to restriction and/or | | | | | | | | | | | | |
| Application Papers | | | | | | | | | | | | |
| 9) The specification is objected to by the Examine | r | | | | | | | | | | | |
| 10)☐ The drawing(s) filed on is/are: a)☐ acce | | xaminer. | | | | | | | | | | |
| Applicant may not request that any objection to the | | | | | | | | | | | | |
| Replacement drawing sheet(s) including the correcti | • • • • • • • • • • • • • • • • • • • • | ` ' | | | | | | | | | | |
| 11) The oath or declaration is objected to by the Ex | | , , | | | | | | | | | | |
| Priority under 35 U.S.C. § 119 | | | | | | | | | | | | |
| 12) Acknowledgment is made of a claim for foreign | priority under 35 U.S.C. § 119(a) | -(d) or (f). | | | | | | | | | | |
| a) ☐ All b) ☐ Some * c) ☐ None of: | | | | | | | | | | | | |
| 1. Certified copies of the priority documents | s have been received. | | | | | | | | | | | |
| 2. Certified copies of the priority documents | s have been received in Application | on No | | | | | | | | | | |
| 3. Copies of the certified copies of the prior | ity documents have been receive | d in this National Stage | | | | | | | | | | |
| application from the International Bureau | ı (PCT Rule 17.2(a)). | , | | | | | | | | | | |
| * See the attached detailed Office action for a list | of the certified copies not receive | d. | | | | | | | | | | |
| | | | | | | | | | | | | |
| Attachment(s) | | | | | | | | | | | | |
| 1) X Notice of References Cited (PTO-892) | 4) Interview Summary | (PTO-413) | | | | | | | | | | |
| 2) Dotice of Draftsperson's Patent Drawing Review (PTO-948) | Paper No(s)/Mail Da | te | | | | | | | | | | |
| 3) Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date 10/11/05,7/12/04. | 5) Notice of Informal Pa 6) Other: <u>alr'a</u> n me | | | | | | | | | | | |
| | | ••• | | | | | | | | | | |

DETAILED ACTION

Status of the Application

Claims 1-40 are pending.

Applicant's election without traverse of Group II, claims 1-40 drawn to a process for producing para-hydroxystyrene with a polypeptide comprising SEQ ID NO: 4, as submitted in a communication filed on 9/25/2006 is acknowledged.

It is noted that there no claim 28 has been presented. Thus, in accordance with 37 CFR 1.126, claims 1-41 have been renumbered 1-40. For example, previous claim 29 is now claim 28, previous claim 30 is now claim 29, etc. Applicant is requested to use the new numbering of the claims in future communications. Also, please note that the claim numbers used in this Office action reflect the renumbering of the claims.

Claims 1-40 are at issue and are being examined herein.

Priority

- 1. Acknowledgment is made of a claim for domestic priority under 35 U.S.C. 119(e) to provisional application No. 60/462827 filed on 4/14/2003, and 60/547170 filed on 2/24/2004.
- 2. Applicant's amendment of the first paragraph of the specification, as filed on 9/25/2006, claiming priority to 60/547170 filed on 2/24/2004 is acknowledged.

Information Disclosure Statement

3. The information disclosure statements (IDS) submitted on 10/11/2005 and 7/12/2004 are acknowledged. The submissions are in compliance with the provisions of 37 CFR 1.97. Accordingly, the information disclosure statements are being considered by the examiner.

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Claim Rejections - 35 USC § 112, Second Paragraph

4. The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

- 5. Claims 7, 17-19, 25, 29, 38-40 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.
- 6. Claims 7 and 29 are indefinite in the recitation of "cell selected from the group consisting of soybean, rapeseed, pepper.....and forage grasses" because the items to select from are not cells but vegetables/fruits/plants. For examination purposes, it will be assumed that the claims refer to cells from those items. Correction is required.
- 7. Claims 17-19 and 39-40 are indefinite in the recitation of "a process according claim 1/20 wherein the para-hydroxystyrene is chemically derivatized in the extractant to form a derivatized compound" for the following reasons. While the preamble in claims 1 and 20 refer to a process for producing para-hydroxystyrene, claims 17-19 and 38-40 are drawn to a process for producing a derivative of para-hydroxystyrene. Thus, the product to be made by the process of claims 1 and 20 is not the same as that of claims 17-19 and 38-40. For examination purposes, it will be assumed that claims 17 and 38 are independent claims directed to a method of producing derivatives of para-hydroxystyrene which incorporate the steps of claims 1 and 20. Correction is required.
- 8. Claim 25 is indefinite in the recitation of "wherein the wildtype host cell is selected form the group consisting of *Lactobacillus plantarum*..." for the following reasons. The wildtype host cell being referred to is the source of the enzyme of SEQ ID NO: 4. According to the specification, the enzyme of SEQ ID NO: 4 is a *B. subtilis* enzyme and not a *Lactobacillus plantarum* enzyme. For examination purposes, no patentable weight will be given to the term "*Lactobacillus plantarum*". Correction is required.

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9. Claim 38 is indefinite in the recitation of "wherein the fermentation medium after step (c) is optionally added back to the biphasic reaction medium" for the following reasons. Step (c) in claim 20 requires contacting the fermentation medium with the enzyme source and extraction of the product (parahydroxystyrene) into the extractant. Step (c) does not require separating the extractant from the fermentation medium. Separation of the two phases occurs in step (d). Thus, the limitation recited in claim 38 is unclear and confusing because the fermentation medium is still part of the reaction mixture after step (c). Only after separation of the phases has occurred, one can recycle the fermentation medium. For examination purposes, it will be assumed that the claim recites "wherein the fermentation medium after step (d) is optionally added back to the biphasic reaction medium". Correction is required.

Claim Rejections - 35 USC § 103

- 10. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:
 - (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.
- This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary.

 Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).
- 12. Claims 1-3, 8-14 are rejected under 35 U.S.C. 103(a) as being unpatentable over Cavin et al. (Applied and Environmental Microbiology 64(4):1466-1471, 1998) in view of Lee et al. (Enzyme and

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Microbial Technology 23:261-266, 1998; cited in the IDS and the specification). Cavin et al. teach the purification and characterization of the B. subtilis decarboxylase of SEQ ID NO: 4 of the instant application. Cavin et al. teach that the decarboxylase of SEQ ID NO: 4 uses p-coumaric acid (also known as para-hydroxycinnamic acid), ferulic acid and caffeic acid as substrates (Abstract; Table 1). Decarboxylation of p-coumaric acid would produce para-hydroxystyrene. Cavin et al. uses B. subtilis crude cell extracts for enzymatic characterization of the enzyme (Table 1). Cavin et al. does not teach production of para-hydroxystyrene in a biphasic medium. Lee et al. teach decarboxylation of ferulic acid to 4-vinylguaiacol by whole cells of B. pumilus that produce a ferulate decarboxylate in an aqueous/organic solvent two-phase system (Abstract). Lee et al. also teach the partition coefficient of ferulic acid and 4-vinylguaiacol in various solvents including hexane (Table 1), the enzymatic activity of the decarboxylase contained in whole B. pumilus cells using different solvents including hexane (Table 2), the use of a fedbatch aqueous-organic two phase system to avoid ferulic acid substrate inhibition (page 264, right column), the separation of the phases by centrifugation, isolation of 4-vinylguaiacol by HPLC using a Hypersil C18 resin (page 262, Analytical Methods), and cell harvest by centrifugation (page 262, right column, second full paragraph). Lee et al. teach that the best results were obtained with a twophase system containing equal volumes (50%/50%) of hexane and phosphate buffer (page 264, left column, second full paragraph). Lee et al. do not teach the production of para-hydroxystyrene or the decarboxylase of SEQ ID NO: 4.

Claims 1-3 are directed in part to a method for producing para-hydroxystyrene by providing an enzyme source containing the decarboxylase of SEQ ID NO: 4, wherein said enzyme is contacted with para-hydroxycinnamic acid in a biphasic reaction medium (aqueous/organic solvent), wherein said biphasic reaction medium contains hexane as the organic solvent phase, and wherein said enzyme source is the purified enzyme or a wildtype *B. subtilis* cells. Claims 9-10 are directed in part to the method of claim 1 with the added limitation that the extractant (organic phase) is present in the biphasic medium in

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an amount from 20% to 50% by volume. Claim 8 is directed to the method of claim 1 with the added limitation that the enzyme source is immobilized. Claim 11 is directed in part to the method of claim 1 with the added limitation that the organic phase (extractant) is separated from the aqueous phase by centrifugation. Claims 12-13 are directed in part to the method of claim 1 wherein the enzyme source is recovered from the aqueous phase by centrifugation or filtration. Claim 14 is directed in part to the method of claim 1 wherein para-hydroxystyrene is recovered by adsorption by resins.

It would have been obvious to one of ordinary skill in the art at the time the invention was made to produce para-hydroxystyrene, which is a derivative of 4-vinylguaiacol, using the method described by Lee et al., wherein the enzyme source is immobilized and/or the enzyme source is recovered by centrifugation or filtration, and wherein para-hydroxystyrene is recovered by adsorption by resins (e.g., HPLC). A person of ordinary skill in the art is motivated to produce para-hydroxystyrene in a biphasic medium for the benefit of avoiding substrate and product inhibition, as taught by Lee et al. with regard to a similar decarboxylase from B. pumilus (page 262, left column, lines 2-3, first full paragraph). In the absence of evidence to the contrary, one of skill in the art would expect the decarboxylase of Cavin et al. to also experience substrate and product inhibition. Also, one of skill in the art is motivated to immobilize the enzyme source as immobilization allows for recovery of the enzyme, lower operation costs as enzyme loss is less likely, and potential enzyme stability. There is motivation to recover the enzyme source by centrifugation/filtration as these are easy methods to separate solids from liquids which are well known in the art and also taught by Lee et al. Similarly, there is motivation to use HPLC to isolate para-hydroxystyrene as this is a well known separation method used to isolate a close derivative of para-hydroxystyrene. One of ordinary skill in the art has a reasonable expectation of success at producing para-hydroxystyrene using the method described by Lee et al. for 4-vinylguaiacol with the enzyme of Cavin et al. and para-hydroxycinnamic acid as the substrate in view of the fact that Cavin discloses the enzyme which catalyzes the decarboxylation of para-hydroxycinnamic acid and Lee et al. teach the

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successful use of a biphasic medium with hexane for 4-vinylguaiacol, which is a structurally close derivative of para-hydroxystyrene. Furthermore, one of skill in the art has a reasonable expectation of success at immobilizing the enzyme and/or recover the enzyme source by centrifugation or filtration in view of the fact that (1) enzyme/whole cell immobilization is well-known in the art, as admitted by Applicant (page 20, lines 8-26), and (2) centrifugation/filtration are well known methods of separation. There is a reasonable expectation of success at isolating para-hydroxystyrene by HPLC as a closely related derivative was successfully separated by HPLC. Therefore, the invention as a whole would have been prima facie obvious to a person of ordinary skill in the art at the time the invention was made.

Double Patenting

13. The nonstatutory double patenting rejection is based on a judicially created doctrine grounded in public policy (a policy reflected in the statute) so as to prevent the unjustified or improper timewise extension of the "right to exclude" granted by a patent and to prevent possible harassment by multiple assignees. A nonstatutory obviousness-type double patenting rejection is appropriate where the conflicting claims are not identical, but at least one examined application claim is not patentably distinct from the reference claim(s) because the examined application claim is either anticipated by, or would have been obvious over, the reference claim(s). See, e.g., In re Berg, 140 F.3d 1428, 46 USPQ2d 1226 (Fed. Cir. 1998); In re Goodman, 11 F.3d 1046, 29 USPQ2d 2010 (Fed. Cir. 1993); In re Longi, 759 F.2d 887, 225 USPQ 645 (Fed. Cir. 1985); In re Van Ornum, 686 F.2d 937, 214 USPQ 761 (CCPA 1982); In re Vogel, 422 F.2d 438, 164 USPQ 619 (CCPA 1970); and In re Thorington, 418 F.2d 528, 163 USPQ 644 (CCPA 1969).

A timely filed terminal disclaimer in compliance with 37 CFR 1.321(c) or 1.321(d) may be used to overcome an actual or provisional rejection based on a nonstatutory double patenting ground provided the conflicting application or patent either is shown to be commonly owned with this application, or claims an invention made as a result of activities undertaken within the scope of a joint research agreement. Effective January 1, 1994, a registered attorney or agent of record may sign a terminal disclaimer. A terminal disclaimer signed by the assignee must fully comply with 37 CFR 3.73(b).

14. Claims 1-2, 4-14 are provisionally rejected on the ground of nonstatutory obviousness-type double patenting as being unpatentable over claims 1-14, 17-19 of copending Application No. 10/439478 in view of Lee et al. (Enzyme and Microbial Technology 23:261-266, 1998; cited in the IDS and the specification). Although the conflicting claims are not identical, they are not patentably distinct from each other for the following reasons.

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Claims 1-14, 17-19 of U.S. Application No. 10/439478 are directed in part to a method for the production of para-hydroxystyrene, wherein said method requires cultivation of specific bacterial, yeast, fungi, and plant recombinant cells, wherein said recombinant cells comprise at least one gene encoding a polypeptide having para-hydroxycinnamic acid decarboxylase activity, wherein said polypeptide comprises SEQ ID NO: 4 of the instant application (SEQ ID NO: 6 in U.S. Application No. 10/439478), and wherein said cells further comprise at least one gene encoding a polypeptide having tyrosine/phenylalanine ammonia lyase activity and cinnamate 4-hydroxylase activity. The specification of U.S. Application No. 10/439478 does not contemplate the claimed method to be practiced in a biphasic medium.

Lee et al. teach decarboxylation of ferulic acid to 4-vinylguaiacol by whole cells of *B. pumilus* that produce a ferulate decarboxylate in an aqueous/organic solvent two-phase system (Abstract). Lee et al. also teach the partition coefficient of ferulic acid and 4-vinylguaiacol in various solvents including hexane (Table 1), the enzymatic activity of the decarboxylase contained in whole *B. pumilus* cells using different solvents including hexane (Table 2), the use of a fedbatch aqueous-organic two phase system to avoid ferulic acid substrate inhibition (page 264, right column), the separation of the phases by centrifugation, isolation of 4-vinylguaiacol by HPLC using a Hypersil C18 resin (page 262, Analytical Methods), and cell harvest by centrifugation (page 262, right column, second full paragraph). Lee et al. teach that the best results were obtained with a two-phase system containing equal volumes (50%/50%) of hexane and phosphate buffer (page 264, left column, second full paragraph). Lee et al. do not teach the production of para-hydroxystyrene or the decarboxylase of SEQ ID NO: 4.

Claims 1-2 are directed in part to a method for producing para-hydroxystyrene by providing an enzyme source containing the decarboxylase of SEQ ID NO: 4, wherein said enzyme source is contacted with para-hydroxycinnamic acid in a biphasic reaction medium (aqueous/organic solvent), wherein said biphasic reaction medium contains hexane as the organic solvent phase, and wherein said enzyme source

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is a recombinant cell that produces the decarboxylase of SEQ ID NO: 4. Claims 4-7 are directed to the method of claim 1 wherein the recombinant host cell is a particular type of bacterial cell, yeast cell, or plant cell. Claim 8 is directed to the method of claim 1 with the added limitation that the enzyme source is immobilized. Claims 9-10 are directed in part to the method of claim 1 with the added limitation that the extractant (organic phase) is present in the biphasic medium in an amount from 20% to 50% by volume. Claim 11 is directed in part to the method of claim 1 with the added limitation that the organic phase (extractant) is separated from the aqueous phase by centrifugation. Claims 12-13 are directed in part to the method of claim 1 wherein the enzyme source is recovered from the aqueous phase by centrifugation or filtration. Claim 14 is directed in part to the method of claim 1 wherein parahydroxystyrene is recovered by adsorption by resins.

It would have been obvious to one of ordinary skill in the art at the time the invention was made to produce para-hydroxystyrene, which is a derivative of 4-vinylguaiacol, using the method described by Lee et al., wherein the enzyme source is immobilized and/or the enzyme source is recovered by centrifugation or filtration, and wherein para-hydroxystyrene is recovered by adsorption by resins (e.g., HPLC). A person of ordinary skill in the art is motivated to produce para-hydroxystyrene in a biphasic medium for the benefit of avoiding substrate and product inhibition, as taught by Lee et al. with regard to a similar decarboxylase from *B. pumilus* (page 262, left column, lines 2-3, first full paragraph). In the absence of evidence to the contrary, one of skill in the art would expect the decarboxylase of SEQ ID NO: 4 to also experience substrate and product inhibition. Also, one of skill in the art is motivated to immobilize the enzyme source as immobilization allows for recovery of the enzyme, lower operation costs as enzyme loss is less likely, and potential enzyme stability. There is motivation to recover the enzyme source by centrifugation/filtration as these are easy methods to separate solids from liquids which are well known in the art and also taught by Lee et al. Similarly, there is motivation to use HPLC to isolate para-hydroxystyrene as this is a well known separation method used to isolate a close derivative of

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para-hydroxystyrene. One of ordinary skill in the art has a reasonable expectation of success at producing para-hydroxystyrene using the method described by Lee et al. for 4-vinylguaiacol with the polypeptide of SEQ ID NO: 4 and para-hydroxycinnamic acid as the substrate in view of the fact that Lee et al. teach the successful use of a biphasic medium with hexane for 4-vinylguaiacol, which is a structurally close derivative of para-hydroxystyrene. Furthermore, one of skill in the art has a reasonable expectation of success at immobilizing the enzyme and/or recover the enzyme source by centrifugation or filtration in view of the fact that (1) enzyme/whole cell immobilization is well-known in the art, as admitted by Applicant (page 20, lines 8-26), and (2) centrifugation/filtration are well known methods of separation. There is a reasonable expectation of success at isolating para-hydroxystyrene by HPLC as a closely related derivative was successfully separated by HPLC. Therefore, the invention of claims 1-14, 17-19 of copending Application No. 10/439478 in view of Lee et al. render the invention of claims 1-2, 4-14 of the instant application obvious to one of ordinary skill I the art.

This is a <u>provisional</u> obviousness-type double patenting rejection because the conflicting claims have not in fact been patented.

Conclusion

- Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PMR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).
- 16. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Delia M. Ramirez whose telephone number is (571) 272-0938. The examiner can normally be reached on Monday-Friday from 8:30 AM to 5:00 PM. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Dr. Ponnathapura Achutamurthy can be reached on (571)

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272-0928. Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (571) 272-1600.

Delia M. Ramirez, Ph.D.

Patent Examiner Art Unit 1652

DR

November 17, 2006

| Q9khj0 lactobacill | Q9khi9 lactobacill | Q9khi6 lactobacill | Q9khjl lactobacill | Q6db32 erwinia car | Q9kpx2 vibrio chol | Q9khj2 lactobacill | Q9r4c1 bacillus pu | Q9r4w3 pseudomonas | Q4ih86 gibberella | Q2u718 aspergillus | Q4p8s8 ustilago ma | | Q6fsx2 candida gla | Q6b961 candida gla | 067763 aquifex aeo | Q9agx3 vibrio chol | Q50s17 entamoeba h | Q8tht9 methanosarc | | Q321t4 brachydanio | Q6f0t4 mesoplasma | Q5kyp9 geobacillus | Q46di3 methanosarc | Q4er00 listeria mo | Q537q2 pyrrhobryum | Q5t089 homo sapien | Q8ww30 homo sapien | Q50r13 entamoeba h | Q9h852 homo sapien |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| Q9KHJ0_LACPA | Q9KHI9_LACPE | Q9KHI6_LACBR | Q9KHJ1_9LACO | Q6DB32_ERWCT | PADC VIBCH | O9KHJ2 LACHI | O9R4C1_BACPU | O9R4W3_PSEFL | Q4IH86_GIBZE | Q2U7L8_ASPOR | Q4P8S8_USTMA | Q43KC0_9CHLB | Q6FSX2_CANGA | Q6B961 CANGA | RPOC AQUAE | Q9AGX3_VIBCH | OSOSL7_ENTHI | Q8THT9_METAC | Q6BIU2_DEBHA | Q32LT4_BRARE | O6FOT4_MESFL | Q5KYP9_GEOKA | : Q46DI3_METBA | Q4ER00_LISMO | Q537Q2_9BRYO | OSTO89_HUMAN | OSWW30 HUMAN | O50R13_ENTHI | 09H852_HUMAN |
| 107 2 | 108 2 | 107 2 | 109 2 | 169 2 | 174 1 | 95 2 | 39 2 | 38 2 | 176 2 | 172 2 | 175 2 | 681 2 | 866 2 | 1504 2 | 1574 1 | 312 2 | 1588 2 | 379 2 | 540 2 | 462 2 | 527 2 | 1044 2 | 379 2 | 400 2 | 196 2 | 350 2 | 350 2 | 366 2 | 497 2 |
| 55.3 | 53.7 | 52.9 | 52.6 | 52.3 | 47.5 | 37.3 | 21.4 | 19.6 | 15.6 | 13.0 | 12.8 | 10.7 | 10.4 | | 10.4 | | 9.8 | | 9.6 | 9.6 | 9.6 | 9.6 | 9.5 | 9.5 | 9.5 | 9.5 | 9.5 | 9.5 | 9.5 |
| 488 | 474 | 467 | 464 | 461 | 419 | 329 | 189 | 172.5 | 138 | 115 | 112.5 | 94 | 92 | 92 | 91.5 | 86.5 | 86.5 | 85 | 82 | 84.5 | 84.5 | 84.5 | 84 | 84 | 83.5 | 83.5 | 83.5 | 83.5 | 83.5 |
| 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | 28 | 59 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 47 | 42 | 43 | 44 | 45 |

NUCLEOTIDE SEQUENCE [GENOMIC DNA]

STRAIN=168;

ALIGNMENTS

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characterization of phenolic acid decarboxylase from Bacillus
                                                                                                                                                                                                                                       Cavin J.-F., Dartois V., Divies C.; "Gene cloning, transcriptional analysis, purification, and
                                                                                                                                            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND CHARACTERIZATION.
                                                                              07-MAR-2006, entry version 37.
Phenolic acid decarboxylase (EC 4.1.1.-) (PAD).
Name=padC; Synonyms=pad; OrderedLocusNames=BSU34400;
                                             integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                Appl. Environ. Microbiol. 64:1466-1471(1998).
[2]
                PRT; 161 AA.
                                                                                                                                                                                                        STRAIN=168;
MEDLINE=98207851; PubMed=9546183;
                                                               sequence version 1.
                STANDARD;
                                                                                                                             Bacillus subtilis.
                                                                                                                                                          NCBI_TaxID=1423;
                                             10-OCT-2002,
                                                               01-JUL-1997,
              PADC_BACSU
007006;
PADC_BACSU
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RK STANN=168 (With Standard St
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Distributed under the Creative Commons Attribution-NoDerive License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: Catalyzes the decarboxylation of phenolic acids such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 extracts from caffeic acid-induced cells exhibited lower activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on the three acids, which indicates that caffeic acid could be a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- INDUCTION: By ferulic, p-coumaric and caffeic acids. Cells
                                                                           Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Optimum temperature is 40-45 degrees Celsius;
                                                                                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    less efficient inducer.
-!- SIMILARITY: Belongs to the padC family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ferulic, p-coumaric and caffeic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: Homodimer (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Temperature dependence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Optimum pH is 5.0;
                                                     Denizot F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subtilis.";
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61 SWTEPTGTDVSLNFMPNEKRMHGIIFFPKWVHEHPBITVCYQNDHIDLMKESREKYETYP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SWTEPTGTDVSLNFWPNEKRMHGIIFFPKWVHEHPEITVCYQNDHIDLMKESREKYETYP 120
                                                                                                                                                                                                                                                                                                                                               1 MENFIGSHMIYTYENGWEYEIYIKNDHTIDYRIHSGMVAGRWVRDQEVNIVKLTEGVYKV 60
                                                                                                                                                                                                                                                                                                                                                                1 MENFIGSHMIYTYENGWEYEIYIKNDHTIDYRIHSGWVAGRWVRDQEVNIVKLTEGYYKV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerive License
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22947447; PubMed=12819959; DOI=10.1007/s00253-003-1371-y; Prim N., Pastor F.I.J., Diaz P.; Blochemical studies on cloned Bacillus sp. BP-7 phenolic acid
                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                            Score 882; DB 1; Length 161;
Pred. No. 1.8e-70;
                                                                                                                                                                                                       1 161 Phenolic acid decarboxylase.
/FIId=PRO_0000108125.
161 AA; 19077 MW; BAP73F679D0FC313 CRC64;
                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacilius sp. BP-7.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=126733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 KYVVPEFAEITFLKNEGVDNEEVISKAPYEGMTDDIRAGRL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2002, integrated into UniFrotKB/TrEMBL.
01-OCT-2002, sequence version 1.
07-FEB-2006, entry version 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8KXX7_9BACI PRELIMINARY; PRT; 161 AA.
AC Q8KXX7;
AC Q8KXX7;
EMBL; AF017117; AAC46254.1; -; Genomic_DNA.
EMBL; 294043; CAB068020.1; -; Genomic_DNA.
EMBL; 299121; CAB15445.1; -; Genomic_DNA.
PIR; D69671; D69671.
                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  decarboxylase PadA.";
Appl. Microbiol. Biotechnol. 63:51-56(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ492219; CAD37333.1; -; Genomic_DNA.
                                                                                                                                                                                         Complete proteome; Decarboxylase; Lyase.
CHAIN 1 161 Phenolic ac
                                                                GenomeReviews; AL009126_GR; BSU34400.
Subtilist; BG12433; padC.
BioCyc; BSU31423:BSU347-MONOMER; -.
InterPro; IPR009729; PA_decarbox.
Pfam; PF05870; PA_decarbox; 1.
PIRSF; PIRSF011561; PAD; 1.
                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                             100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phenolic acid decarboxylase.
                                                                                                                                                                                                                                                                                                             Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=padA;
                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                            Query Match
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